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  Intellegenetics
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FastDB - Fast Pairwise Comparison of Sequences

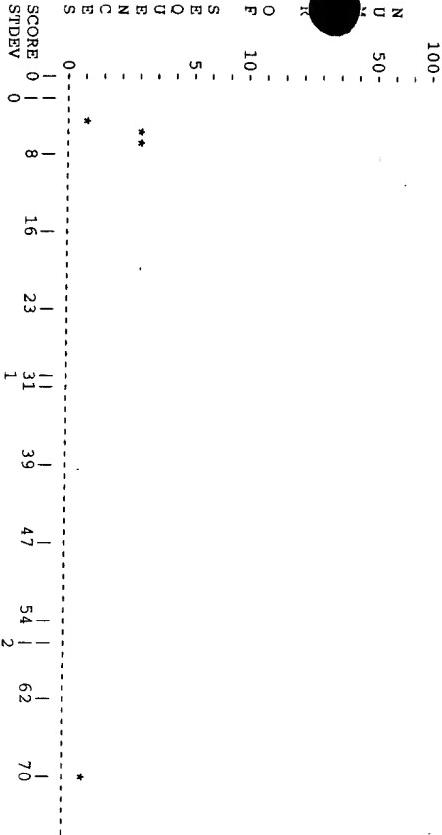
Release 5.4

Results file 09972467-2-509-578-ab037733.res made by delaval on Thu 20 Jun 102 6:17:05-

Query sequence being compared: US-09-972-467-2 (509-578)
Number of sequences searched: 6
Number of scores above cutoff: 6

Results of the initial comparison of US-09-972-467-2 (509-578) with:

File : ab037733.seq



Sequence Name	Description	Length	Score	Score	Sig.	Frame
1. ab037733	TOIG of: ab037733	check: 480	1712	70	70	2.07

The list of other best scores is:

Sequence Name	Description	Length	Score	Score	Init.	Opt.	Sig.	Frame
2. ab037733	TOIG of: ab037733	check: 480	1711	7	14	-0.35	6	
3. ab037733	TOIG of: ab037733	check: 480	1712	7	12	-0.35	4	
4. ab037733	TOIG of: ab037733	check: 480	1711	6	13	-0.38	5	
5. ab037733	TOIG of: ab037733	check: 480	1713	6	12	-0.38	1	
6. ab037733	TOIG of: ab037733	check: 480	1712	5	11	-0.42	3	

1. US-09-972-467-2 (509-578)

ab037733 TOIG of: ab037733 check: 4803 from: 1 to: 5139

TOIG of: ab037733 check: 4803 from: 1 to: 5139

LOCUS AB037733 5139 bp mRNA linear PRI 14-MAR-2000
DEFINITION Homo sapiens mRNA for KIAA1312 protein, partial cds.
ACCESSION AB037733
VERSTON AB037733.1 GI:7242978

SOURCE Homo sapiens brain cDNA to mRNA, clone.lib:pBluescriptII SK plus
ORGANISM Homo sapiens

REFERENCE 1 (sites)
AUTHORS Nagase,T., Kikuno,R., Ishikawa,K.I., Hirose,M. and Ohara,O.
TITLE XVI. The complete sequences of 150 new cDNA clones from brain which
code for large proteins in vitro

JOURNAL DNA Res. 7 (1), 65-73 (2000)
JOURNAL 2018126
MEDLINE
REFERENCE 2 (bases 1 to 5139)
AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2000) osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1523 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:ccnainfo@kazusa.or.jp;
URL: http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)

FEATURES Location/Qualifiers
source 1. .5139
/organism="Homo sapiens"
/clone="fhl1767"
/clone_id="fhl1767"
/tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
gene 1. .4417
/genes="KIAA1312"
/<..-.4417
/genes="KIAA1312"
/note="Start codon is not identified."
/codon_start=2
/product="KIAA1312 protein"
/protein_id="BA9250_1"
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/translation="NSEHTAVTISLCSGMUGLTFRSHGDDYTFEPLSMSDEODEEFOK
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LATEAFSAVGNKDNTRREKRTHRRTRKFLSYPREVEVLWADNRKVSHGENQHVT
TMSITASYKDPSTGNLNLIVNVLIVNVLIVNEQGPSTSFRAOFTLNEQWOKHSNS
PGGIHDHTAVLUTDRCRAHDKCQLGIALENEQGPSTSFRAOFTLNEQWOKHSNS
ELGHVNMPHDNNKCKEENSKSPORMVATLNFYTPMWSKSKRYVTEFLDYG
ECLLNPRSPESRVPPLPVOLPAGTCPEPGHCKYGFCPVQCMPLFPGSOPYMMQRWICNNNGVH
KGCRTOHTPPADGTCPEPGHCKYGFCPVQCMPLFPGSOPYMMQRWICNNNGVH
KTAECRNRCPKNGKCYGGRMKFKSCIEPKQKQRDRQCAHDFGKHTNG
LLPNVNRWPKYSLIMKDRKLCFCAVAGNTAYQDRLTDGTCGQDQTNIDCVQGLC
RQAGCHVHLNSKARRDKCGVGGDNSSCKTIVAGTNTVNGVNTVVRPAGRNIDVR

The scores below are sorted by initial score.
Significance is calculated based on initial score.

Scores:

Mean	16	Median	7	Standard Deviation	26.06
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Times:

00:00:00.00 CPU

Total Elapsed

Number of residues: 10271
Number of sequences searched: 6
Number of scores above cutoff: 6

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 10% similar sequence to the query sequence was found:

OHSFGETDDNYIALSSRGEFLINGNNEVVMKARETRIGNAVENSGSETAVERIN
 STDIEOELLLOVLSVKGKVNPDYRSTNPIDPKQFYWNHGPWQACKSKCQGER
 KRKLVCRTSRSQDLVNSQPCPDRFLCPQHTEPQGKCDLWRHVASRSECQAC
 TLDIYAKKSRLDEKTDGGFESSHPSNRKCSGCCNTGWRVSAWTECKSCD
 GGTORRAZCVNTNDVLUDSKCQKTCVQIQRCSEFFCPQWNSQGDWBCBLVCGKH
 KHRWACOGEDRINDMDPQDCEPDKPTSMOTCQHPCWQAGWQACSGYQOL
 AVKLIGTMSVVDNDCHATRTPDQCELPSCHPAPAPERTRSYASPRTOWR
 GSWTPCSACAGKGTMRVYSCRDNGSVADASCATLRPVAKECBSPVCGWALD
 WSSCVTCCGGRATRQMVNVSHVTSQEDDYLTETDQCSMSPCPQRTPSGL
 AOHFQEYDPRPASPSITHVLLGGNQWITPGWACSSCTAGGSQRVVCQDENGY
 ANDCVERIFIDEQRAESCPQAWYANGECTKLGGEITRULVCSNGERFPDL
 SCIELDKPDRQECNTHACPDAWSTPWWSCS
 DYCBLAKKGHRKCRGGCKPKWAGANWSQCSVCGRGQHQGCQGTHKARETE
 CNPVTPEERBDQGCPCLYTWRAEEMEBCTKTPEGESRYRKVVCVDDNKNEVHGA
 CDPVKRPVRESLQPCSYWVSPWEL"

 BASE COUNT 1471 a 1112 c 1362 g 1194 t
 ORIGIN 1112 c 1362 g 1194 t

 AB037733 Length: 5139 June 20, 2002 06:02 Type: N Check: 4803 .

 Initial Score = 70 Optimized Score = 70 Significance = 2.07
 Residue Identity = 100% Matches = 70 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

 Translation Frame= 2

 NSEHTAVISLCGMLGTFRSHGDYFTPLQSMDQEDEEONKPHIYRRAPOREPSTGRHACDTSEHKN
 10 30 40 50 60 70

 RHSKDKKKTRARKWGERINLAGDVAAALNSGLATEAFASAYGNKIDNTREKRRTKFLSYPRFEVILWAD
 20 90 100 110 120 130

 NRMVSYHGENLQHYLTLMSIVASIKDPSIGNLINVIVNLVIVHQDQPSISFNQATTLNKNFQWQHSK
 150 160 170 180 190 200

 NSPGQIHHDATVLLTRQDTCRAHDKDCTIGLARLGTICDPYRCSISISEDSGLSTAFTIAHELGHVFMMPHDD
 220 230 240 250 260 270

 220 230 240 250 260 270

 X 10

 QLPGIIXNN
 |||||I|||
 NNKCKECEGVSPQHVMAPTLNFYINPMWMSKCSRKYITEFLDGYGECLINEPESRPYPLPVOLPGIIXNN
 290 300 310 320 330 340

 KOCLBLIGFGGSQVCPYMMQCCRLLACNNNGVHKCRTCQHFWADGTECEPGKHCCKYFCV
 290 300 310 320 330 340

 KQCELEIFPGSQVCPYMMQCCRLLACNNNGVHKCRTCQHFWADGTECEPGKHCCKYFCV
 370 380 390 400 410 420

 WGSNSPFGCSRTGGGIKTAIRECNRPEPKNGKCYGRRMKFKSCNTREPLCKQKDRFRDEOCAHFQKHF
 440 450 460 470 480 490

 NINGLPLPNTRWVPRYKSGILMKDRCKLFCRVAGNAYQYQDRVIDGTPCGQGDNDICVQGLCIRQAGCDHVLN
 510 520 530 540 550 560

 SKARRDKCQGNGNSCKVKAHGFTNTVHYGNTVVRIPAGATNIDVROHSFGETDDNYIALSSRGEFL
 580 590 600 610 620 630

 LNGNFVVTMAKRETRIGNAVEYSGESTAVERINSTDRTEQELLJLQVLGVKLYNPDVYRYSNIPIDKPOQ
 650 660 670 680 690 700

 FYWNSHGPWQACSKRCPQGGERKRLVCTRESQDLTVSDQRCDRLPQPHTEPCGTCDCDLRWVHVASRSECQA
 730 740 750 760 770 780

 CGLGYRTLDITYCAKVSRLCKTEKVDFGFCSSHPKPPSNREKCGSECNTGWRVSAWTECSKSCDGTTORRA
 800 810 820 830 840 850

 ICVWTRRDVLDDSKCCTHQEVTLQCSSEPCPQWNSQGDWSECLYTCGKKGKHHVWCOFGEDRINDMDP
 870 880 890 900 910 920

 •T•SMQTCOPECASWQAGPWGCGSVCQGQYQJLRAVKCITGTYMSVVDNDNQATRPTDQDCELPSCH
 940 950 960 970 980 990

 1000

KTAIRECNREBPKNGKRYCGRMRKFKSNCNPCEPLKQKRDFRDECACHEFGKHEWING	50	60
LIPPNWVKYPSGTMKDRKLFCRAGNTAQLPQDRLVDRYDTCGQDNTDCYGLC		
RQAGCDHVLSNSARRDRKCGVGCGDNSSCKTVAFTGTVNHTVWVTPAGATNDVR		
QHSFSCETDDNNYLAUSSKGEFFLNGNFMVWMAKEIRIGANVWEYSGETAVERIN		
STDREFOELLIVLWVSGKLDPKIDNPFSNFPIEDKOPFWNSHPEWPOACSKPCOGER		
KRKLVCTRESQDLTISDQCDRLPQGHTEPPCGTDCDLMWHASERSECSCAQCGLGR		
TLDIYCAVSRLDGKTRVKDGFCSHPSKNSREKSCGECHGWRWYSAWECSEKSCD		
GTTORRRAICVTRNTRVLQDSDKTHOEKVTRFORCEEFPCPOWKSGDWSECLWTCKGH		
KHRQWCOFGEDRLNDRCMCPTEPKSMQTCQEGAWQMGWGCVCQGQQLR		
AVKCCTGTYMSVVDMDNCNATRPTMTODEBLPSCHPPAPETRSTYARPTWRF		
GSWTPROSATCGCRATROVMCVNSWHDILREDDOYIPEPDODCNSPCPORTPISGL		
AQHPFOMEDYPRSRASPSRTVWLGGKWRUTPGWAGASSTTAGSQRVVKVQDENYT		
ANDCVERTKPPQRACESGRPSQWAGNGEBCKGKLGGRTRLYVCORNGERPDLL		
SCELDKPPDRCNPHACPAHDAMSTGPNSCSVSGRRGHKRNVYCMKGSHLES		
DICKHIAKPHCRKGRGCRKACADACQSVSGVQDGRHVGQDIGHKJARTE		
CNPYTRPESERDCQGRCPYLTVWRAEWOCRGKTCGEGSRVYKVVCDINNEVHGR		
CDYSPKPYDRECSLQPECYWITGEWSEYPSWEL"		
BASE COUNT ORIGIN	1471 a	1112 c
Length: 5139 June 20, 2002 06:02 Type: N Check: 4803 ..		
Residue Identity = 21% Optimized Score = 14 Significance = -0.35		
Gaps = 29 Conservative Substitutions = 20 Mismatches = 46		
Translation Frame= 6		
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210 220 230 240 250 260 270 280		
LVFWVVIHTHHLAVPGAFAGLGAFLPFLCPSPSVEGTWWLAVAFLRLRGWVVALGLSGVWALGCSIDLTAHMPLL		
290 300 310 320 330 340 350		
YASATGHRALTPSASPFGASSSALSVPWMLSQVLTWVITFXMASIFCHAVNLISLFLMPSTTRDTRAPRST		
360 370 380 390 400		
PCSVVWTSMCVTLTIGRIFTNAQTQWKPFTVQPLTDHQCSVASTTOLSLSPVATSLPRLTRAGFTGSSL		
430 440 450 460 470 480 490		
IRFVSLHHTVCGVSVIFLTYNTPLGSASTGTGTCSPGASSPLVSTERHMGAGAGAPGTIVLILEGVLSAT		
500 510 520 530 540 550 560		
VWGPLRRAWXHGTVLVSFWIDILVWLTIDHVVTVWDTHILPGLCPTLPTGCHRARAPVQGLFLPTGCHRFFLC		
570 580 590 600 610 620 630		
HWSRGSTGTLVSHRAILISADDVSHPGFPPTSGXAWGRPRPKSPLSGWMTVCASPRFRGSSWGRMTXWXFTV		
650 660 670 680 690 700 710		
GISWSSCCITVIVVYHXHISPNDAFHCSXVLVSLSTDALSPGTRLPGCTFRLTLSHRCWGLGRVTHSIX		
720 730 740 750 760 770 780		
SIFTKLTPDVLVLMPSFSGDQALXVSRFLWRELATAPLNGNELLMCAFAVIQVITISGIDTNSPSPLGPTV		
790 800 810 820 830 840 850		
TAFTXTPSPGRIAPATRVFFXAFTVVAWFGMAAKTITIULSLPIQATFGTVQCAVITQATGTTFTPAG		
860 870 880 890 900 910 920		
NMPPOVTVCTGFSNVSLIGQPIASLIRNNSKLIRPGANKFSFPFLAGFTACLPWPMVWPVKLRFNFNNW		
930 940 950 960 970 980 990 1000		
ITERAYIGVWVOLSHRQNKKQFLNAINCIVNSVNGSLGTVLHISIPMANFPFGHCNDKNSIXOEEFTFAAX		
1010 1020 1030 1040 1050 1060 1070		
SVVVIVCFPXEVLPHINGSTSWNSDHISIVTIMCICKSCHOFAXRITIATNTPTFSTPFGFXVNMASSL		
1080 1090 1100 1110 1120 1130 1140		
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/ab_xref="taxon:9606"		
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/tissue_type="brain"		
/clone_id="pBluescriptII SK plus"		
1. . 4417		
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note="Start codon is not identified."		
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/protein_id="BA92550.1"		
PAKALDTDIICVLA 1150 1160 1170 1180 1190 1200 1210		

/db_xref="GI_7242979"
 /translation="NSEHTAVISCSGMLGTFRSHGDYFTEPLQSMDEQEDEEONK

PHIYRSRSPORESTPGRHACDUSEKHNRKOKKTRARKGERNTILAGWDALNG

LATEFSAYGKNDTNTREKTRHTRKESYPRFELVYVADNMYSYGENLHTL

TMSIVASYKDPSIGNLNLLVNLVTHNEODGPSISFNAQTTLNFCWQHSNS

PGGIHHDTAVLILTRQDIDRAHKDCDTGIGLAEGTICPYRSOSISESGLSAFTIAH

ELGIVENMPHDNNCKKEGVKSPQHMAPTUNFYTPWMWSKCSRXXJTBELDYG

ECLLINEPESSRPYFLPVQLEGLTINVNPKOCEBLLFGPGSOVCIMMQCRLLCIVNNNGH

KGCRCRQHTWADCTECEGKHCCKGYCPCWEMPVTDGSKWDSWPGTCITCGGI

KTAIRECPNPPEPKINGKVCGRMKPFSCNTPCLKOKRDFECAHDFEKSHTING

LLPAVNRWKRYSGLMKDCKLPCRVAGNATYQLRKVIDETPCGDDINDTCVOCG

RQACCDHVINSKARSKDRDNCRDPEKPTKNTQCPCEASWACQPGC5VTGQYLR

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STDRIEQEELLQULVSLGKDNPQYVMMAKRETRIGNAVVEVSSEPAVERIN

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AVKUIGTGMWSVVDNDENAAATRPTDQPLSPCHPPAETRSTYSAFRTORE

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WSSCSVTCQGRATRQVMCNUFSDHVIDSECODYLIFETODCSMSPCPORTPDGL

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ANDCVERTRKPDREGRACRSCPCWPMGNGTCKLGGJIRPLVCGCNGT

SCELDKPDRDENTHACPDHDAMSTGWPSWSSGSVSGRRGHQHORNVYCMADGSHIES

DYCKHLAKEHGHRGRGCRGCRPKWAGQSCSVSCGKVQHQHVGQCOIGTICARTE

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BASE COUNT

ORIGIN

AB037733 Length: 5139 June 20, 2002 06:02 Type: N Check: 4803 ..

Initial Score = 7 Optimized Score = 12 Significance = -0.35
 Residue Identity = 20% Matches = 16 Mismatches = 40
 Gaps = 24 Conservative Substitutions = 0
 Translation Frame= 4

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POBTEHEHQGPVLHAASCGQACVHLHSSRGSLRSITQSLQSKSGNRSPLDXOTTSVLMLPPPHSLVHSPOLPXA

420 430 440 450 460 470 480

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 490 500 510 520 530 540 550

XSSFWKGCXAKPLSGVLUXHGDMEQSQWSVSGTXSMWSHLSRITWSLXLTHTCRVALPCPOVTHQELQSKAF

560 570 580 590 600 610 620

HPQGPVTEHSSATGRLGRAQALSSATEPEFSSRQLTYLIRVPPQVAEHGQDPRNRRHWIGALYVLLVSGA

630 640 650 660 670 680 690

AGGGXHGNQSWSVGLVAALQSLSSSTDXVPMMHFTALSWYPCCPQVTLHCPQGPAQDAHSGCXQVCID

710 720 730 740 750 760 770

VGLVSGSHLSFNRSRPNXHQTWRCCLCPPQVTKNSDQSPDPHCQGQNSHLXWMTFSXCVHLLSSSFVR

780 790 800 810 820 830 840

LTOQIALLWVPPSOLFEHHSVQAEXROPVVLHSPEHFRSLGLGWLQKPSSTFSVFPSSLLYLAQXMSNRX

850 860 870 880 890 900 910

PRPHWALHSLLATCHRSQSVQGWSLWQTSRFRPSMQGLIACHGPXL

920 930 940 950 960 970 980

FOXNCXGLSSIGLILKEXRTSGIYNFTDKTYSKSSCSMRSELVLLSTAVSDPLYSTAFTPMRISLLATVTK
 990 1000 1010 1020 1030 1040 1050

FPPSKNSPLLDKAKYLSVSSPEKICCRCSILVAPGIRTVLXPXCTVLNVPAVTHHEELSPQPTPHSL

1070 1080 1090 1100 1110 1120 1130

*RAFEKTXSHPACROFWTQISFVSPQGVPSITLSRXXXAVPATLQNLNHSRSTIRIPIPLYLGORTIGR
 1140 1150 1160 1170 1180 1190 1200

PIMLKCFPSXAHSSRSRSCIRRHGSVLDNLFFILRPTQVPPFFGSGLHSRMAVLMPPHVLEOPVKGL
 1210 1220 1230 1240 1250 1260 1270

X
 QLPGLYLN
 |||
 OLPQDPSSVGTTSISLGTQPYLQCCPGSHSVPSNQGVXVRQLPLCTPLTLHQSLRHLICIVHTXPGPKIN
 1280 1290 1300 1310 1320 1330 1340 X

10 20 30 40 50 60 70
 SHCLETFLXIMPGS-----WIGKGXGLDSLGSLSKHSRXPVSKNSVYFLRFHDHQGLVX
 1350 1360 1370 1380 1390 1400 X

GAMTCWGLITPSSUHLLSSXGMINTWPSSWATKAVLNPLSLIEQULXGSQMPSSARPKVSHLSXALQI
 1410 1420 1430 1440 1450 1460 1470

SCLVKTAVSXWIPGLPFECCWQKFENVVXALKDMEGPGPSLXITIKFTTILKFPPIGSXLXTEATIDI
 1480 1490 1500 1510 1520 1530 1540 1550
 KVVKIXXRSPWYETILLISATTKUSTNRGDXKKRFLVLUWFLSLVLSVLLPXAENASVAKPLFNATSPARL
 1560 1570 1580 1590 1600 1610 1620 1630
 ILSHFLALVFELLSILCILCSEVSHACLPVGEGLWSLWRLXMMWGFCSSSSSCSIDCGSIKSXPXDR
 1640 1650 1660 1670 1680 1690 1700 1710

NVPSPSEORLMATVCE

4. US-09-972-467-2 (509-578)
 ab037733 TOIG of: ab037733 check: 4803 from: 1 to: 5139

TOIG of: ab037733 check: 4803 from: 1 to: 5139

AB037733

LOCUS AB037733

DEFINITION mRNA for KIAA1312 protein, partial cds.

ACCESSION AB037733

VERSION AB037733.1

KEYWORDS AB037733.1 GI:7242978

SOURCE Homo sapiens brain cDNA to mRNA, clone_1b:pBluescriptII SK plus

clone:fhl1767.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

Authors Nagase,T., Kikuno,R., Ishikawa,K.I., Hiroswa,M. and Ohara,O.

Title Prediction of the coding sequences of 150 new cDNA clones from brain which

code for large proteins in vitro

JOURNAL MEDLINE 2011126

2 (bases 1 to 5139)

Authors Ohara,O., Nagase,T. and Kikuno,R.

Title Direct Submission

Journal Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,

Laboratory of DNA Technology; 1332-3 Yana, Kisarazu, Chiba

292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp)

URL: http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,

Fax,+81-438-52-3914)

FEATURES Location/Qualifiers

1. . 5139

/organism="Homo sapiens"

/db_xref="taxon":9606

/clone="fhl1767"

/tissue_type="brain"

/clone_id="pBluescriptII SK plus"

1. . 4417

/gene="KIAA1312"

<1. . 4417

/gene="KIAA1312"

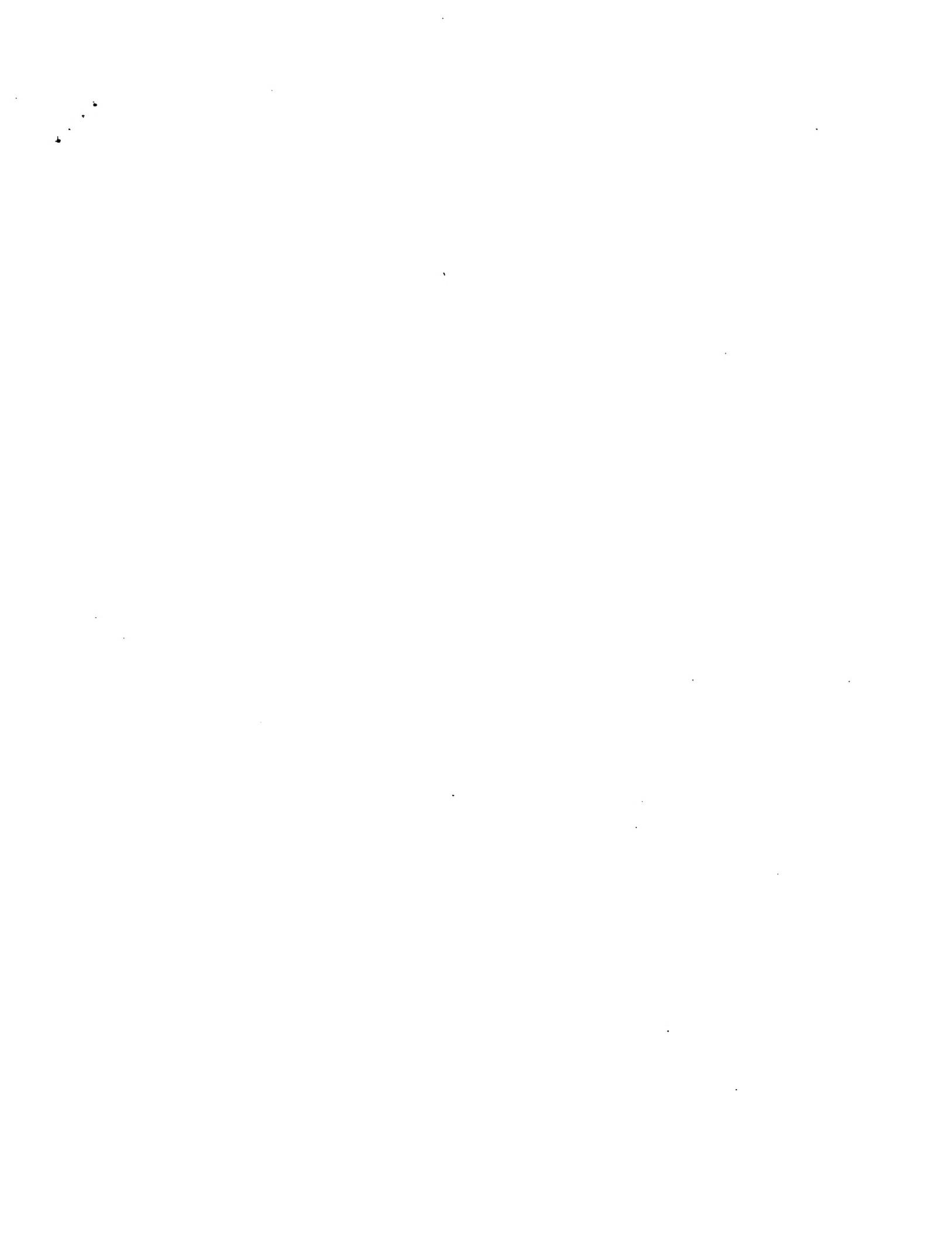
/note="Start codon is not identified."

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 PGGIHDHTAVLTFRDQCRAINDKCDTGLAEIGTCDFPRTSCSISEDGUSTPTIAH
 EIGHVFNMPHDNNCKKEGGPKSPVMAFTNFVTPWMSKRSKRYTCFUDTGY
 KCGCROHTWADGECEPGKNCYKGFCCPMEVDTGSWGSNSPFGCSRCGGI
 KTAIRCRNRPBKNGCYCGRMFKSCNTPECLURKDRFDRCAHEDGKFINING
 LIPNUVRWPKSGTUMDKRCKLCFVGAGNTAQLDRVIDGTFCGDODINDIVQIC
 RQACDYNLSKARRDCCGCGDNNCKVAGNTAQLDRVIDGTFCGDODINDIVQIC
 QHSFSETDDNNLYANLSSKGKEFLINGNFVUTMARETRIGAVVEYSESETAVERIN
 STDRTEQELLIOWLVSKLNUPIVDEYSNTPIDKPOOTWNSHGPWQCSKQGGER
 KRKLVCTRESQDLTSDQRDRFLPQFGHTEPCGIDCJDKWHWASRESEAQGIGYR
 TLDYCAKYSRDGFYKEDFGCFSHPNREICSGCNTGSWRYSAWTEESKSD
 GGTQRERRACVNTNNDVYDLSKTCMOPKVNTRSEPEPOWMGDWSCLVCGKHD
 KHRQWCGFEGDRLNDRCDEPKTSWTCQPECASWGPWQCSVTCGGYQLR
 AVKCTIGTYSWVDDNCATRPTDQCELSCHPPRPAPETRSTVSAPRQWRF
 GSWTPOSATCGKGTMRVYUQNGEVDNSGAGSQQRRVYQNGEVTWNL
 WSCSVTCGCCRATHOMCUNYSHDVIDSECDDYIPEPDQDSMSPQRPIDSL
 AHPFNUEDTRPDRSASKRHLVGLNQWRVNGWACSSCAGSQQRRVYQNGEYT
 ANDCVERTKPDEQDRASCEGCPQWAGYNGEBCGKLGKQHNVYQHAKDSHLES
 SCELDKPPREOONTAHCDDAWSTGPISSCVSGGCHQHNVYQHAKDSHLES
 DICKHLAKPHGHKGRGPWKWAGAWSQSWSGGGRGVQDQHGCGQTHKARETE
 CPyTRPESSENDCCPQRCPLVTRWAEQWECBCTGEGSRSYRKVYKUVCDNNKHNHGAR
 CDWSRPDVDESCLSQPCVWUWIGEWSEVPWEL"

BASE COUNT ORIGIN	1471 a	1112 c	1562 g	1194 t
AB037733 Length:	5139	June 20, 2002 06:02	Type: N	Check: 4803 ..
Initial Score =	5	Optimized Score =	11	Significance = -0.42
Residue Identity =	18%	Matches =	16	Mismatches = 50
Gaps	21	Conservative Substitutions	3	
Translation Frame=				
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GTIVKTRRKKEQENGKELTTLWVTKHQXHTAAQXRHFLMVRITQDQEKRGPTEQGNVFPYHGLXKSWWMDT	80	90	100	110
TEWFHTMEKTENTIFXLQCOLXPISIKIQVLEIXLILXIXFIMNRMGJPUYLMLRQHKTFFASGSIRR	150	160	170	180
TVOVESIMILEXQDRITSALELTNIPXAWNNEPPVPIPEAVLLVKIVDXVQOLLRSPMSWAMCLCLMMT	220	230	240	250
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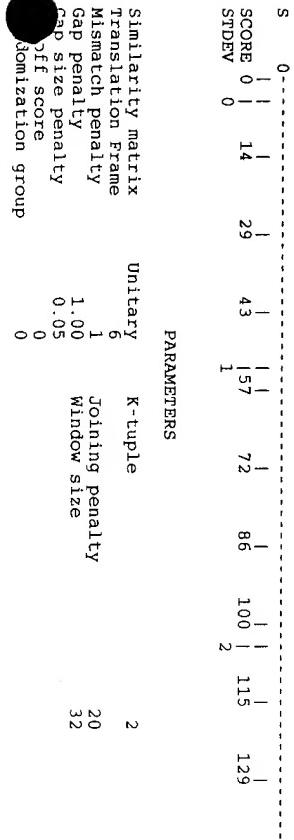
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09972467-2-19-287-ab037733.res made by jdelaval on Thu 20 Jun 102 6:15:26-E
Query sequence being compared: US-09-972-467-2 (19-287)
Number of sequences searched: 6
Number of scores above cutoff: 6

Results of the initial comparison of US-09-972-467-2 (19-287) with:

File : ab037733.seq



Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
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3. ab037733	TOIG of: ab037733 check: 480	1711	8	43	-0.41	6
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1. US-09-972-467-2 (19-287) TOIG of: ab037733 check: 4803 from: 1 to: 5139
TOIG of: ab037733 check: 4803 from: 1 to: 5139

LOCUS AB037733 5139 bp mRNA LINEAR PRI 14-MAR-2000
DEFINITION Homo sapiens mRNA for KIAA1312 protein, partial cds.
ACCESSION AB037733
VERSION AB037733.1 GI:7242978

KWONDS SOURCE Homo sapiens brain cDNA to mRNA, clone-lib:pBluescriptII SK plus
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (sites)
AUTHORS Nagase,T., Rikuno, T., Ishikawa, K.I., Hirose,M. and Ohara,O.
TITLE prediction of the coding sequences of unidentified human genes.
XVI. The complete sequences of 150 new cDNA clones from brain which
code for large proteins in vitro

JOURNAL DNA Res. 7 (1), 65-73 (2000)

MEDLINE 20181126

REFERENCE 2 (bases 1 to 5139)

AUTHORS Ohara,O., Nagase,T. and Rikuno,R.

TITLE Direct Submission

JOURNAL Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,

Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp); URL: http://www.kazusa.or.jp/fnuge/, Tel:+81-438-52-3913, Fax:+81-438-52-3914

FEATURES Location/Qualifiers

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The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

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ORIGIN								
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2. US-09-972-467-2 (19-287)								
TOIG of: ab037733	check:	4803	from:	1	to:	5139	TOIG of:	ab037733 check: 4803 from: 1 to: 5139
LOCUS AB037733	5139 bp	mRNA	linear	PRI	14-MAR-2000		LOCUS	AB037733
DEFINITION Homo sapiens mRNA for KIAA1312 protein, partial cds.							DEFINITION	
ACCESSION AB037733							ACCESSION	
VERSION AB037733.1	GI:7242978						VERSION	
KEYWORDS SOURCE	Homo sapiens brain cDNA to mRNA, clone_lib:pbluescriptII SK plus						KEYWORDS	
ORGANISM Homo sapiens							ORGANISM	
FEATURES	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						FEATURES	
SOURCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						SOURCE	
REFERENCE 1 (sites)	Nagase,T., Kikuno,R., Ishikawa,K.I., Hirose,M. and Ohara,O.						REFERENCE	
AUTHORS	Prediction of the coding sequences of 150 new cDNA clones from brain which						AUTHORS	
TITLE XVI. The complete sequences of 150 new cDNA clones from brain which	code for large proteins in vitro						TITLE	
JOURNAL DNA Res.	Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology, 152-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: cdninfo@kazusa.or.jp), URL: http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913, Fax:+81-438-52-3914)						JOURNAL	
MEDLINE 2018126							MEDLINE	
REFERENCE 2 (bases 1 to 5139)	Ohara,O., Nagase,T. and Kikuno,R.						REFERENCE	
AUTHORS	Direct Submission						AUTHORS	
TITLE JOURNAL	Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology, 152-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: cdninfo@kazusa.or.jp), URL: http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913, Fax:+81-438-52-3914)						TITLE	
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BASE COUNT	1471	a	1112	c	1362	g	1194	t
ORIGIN								
AB037733	Length:	5139	June	20,	2002	06:02	Type:	N
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Translation Frame	=	4						
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FEATURES

- source
- 1. .5139/Qualifiers

REFERENCE

- 1. (sites)

AUTHORS

- Nagase,T., Kikuno,R., Ishikawa,K.I., Hirokawa,M. and Ohara,O.

PREDICTION

- Prediction of the coding sequences of unidentified human genes.

VERSION

- AB037733.1 GI:7242978

KEYWORDS

- Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
- clone:fhl1767.

ORGANISM

- Homo sapiens
- Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

- 2. (bases 1 to 5139)

AUTHORS

- Ohara,O., Nagase,T. and Kikuno,R.

TITLE

- prediction of the coding sequences of unidentified human genes.

JOURNAL

- Journal of Human Genetics (2000) 45: 65-73 (2000)

MEDLINE

- 20181126

FEATURES

- 1. Laboratory of DNA Technology, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Fax:+81-438-52-3913, location+Qualifiers

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 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1. (sites)
 AUTHORS Nagase, T., Kikuno, R., Ishikawa, K.I., Hirose, M. and Ohara, O.
 TITLE Prediction of the coding sequences of 150 new cDNA clones from brain which
 XVII. The complete sequences of 150 new cDNA clones from brain which
 code for large proteins in vitro
 JOURNAL DNA Res. 7 (1), 65-73 (2000)
 MEDLINE 20181126
 REFERENCE 2 (bases 1 to 5139)

REFERENCE
1 (sires)
AUTHORS Negase,T., Kikuno,R., Ishikawa,K.I., Hirosawa,M. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes.
xvi. The complete sequences of 150 new cDNA clones from brain which
code for large proteins in vitro
JOURNAL DNA Res. 7 (1), 65-73, (2000)
MEDLINE 20181126
REFERENCE 2 (bases 1 to 5139)
AUTHORS Ohara,O., Negase,T. and Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2000) Osumi Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail: cdnainto@kazusa.or.jp)
URL: http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
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ab037733 TOIG of: ab037733 check: 4803 from: 1 to: 5139
TOIG of: ab037733 check: 4803 from: 1 to: 5139
LOCUS AB037733 DEFINITION Homo sapiens mRNA for KIAA1312 protein, partial cds.
ACCESSION AB037733 VERSION AB037733.1
KEYWORDS Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
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TOIG of: ab037733 check: 4803 from: 1 to: 5139
LOCUS AB037733 DEFINITION Homo sapiens mRNA for KIAA1312 protein, partial cds.
ACCESSION AB037733 VERSION AB037733.1
KEYWORDS Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus

Thu Jun 20 06:19:50 2002

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Page 8

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1330

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 TITLE Homo sapiens
 JOURNAL JOURNAL OF CLONAL ANALYSIS AND MOLECULAR GENOMICS
 MEDLINE 20181126
 REFERENCE 1 (sites)
 AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
 TITLE Prediction of the coding sequences of unidentified human genes.
 JOURNAL JOURNAL OF CLONAL ANALYSIS AND MOLECULAR GENOMICS
 MEDLINE 20181126
 REFERENCE 2 (bases 1 to 5139)
 AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
 TITLE XVI. The complete sequences of 150 new cDNA clones from brain which
 code for large proteins in vitro
 DNA Res. 7 (1), 65-73 (2000)
 REFERENCE 2 (bases 1 to 5139)
 AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
 TITLE Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
 Laboratory of DNA Technology, 1532-3 Yana, Kisarazu, Chiba
 292-0812, Japan (E-mail: cdnainfo.kazusa.or.jp'
 URL: http://www.kazusa.or.jp/huge/, tel:+81-438-52-3914,
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 TOIG of: ab037733 check: 4803 from: 1 to: 5139
 Locus AB037733 mRNA 5139 bp linear PRI 14-MAR-2000
 Definition Homo sapiens mRNA for KIAA1312 protein, partial cds.
 Accession AB037733 Version AB037733.1 GI:7242978
 Keywords SOURCE
 Organism Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
 clone_fh1767.
 Reference 1 (sites)
 Authors Nagase,T., Kikuno,R., Ishikawa,K.I., Hirose,M. and Ohara,O.
 Title prediction of the coding sequences of unidentified human genes.
 XVI. The complete sequences of 150 new cDNA clones from brain which
 code for large proteins in vitro
 Journal JOURNAL MEDLINE
 DNA Res. 7 (1), 65-73 (2000)
 MEDLINE
 20181126
 Reference 2 (bases 1 to 5139)
 Authors Ohara,O., Nagase,T. and Kikuno,R.
 Title Direct Submission
 Journal Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, China
 Laboratory of DNA Technology, 1512-3 Yana, Kasarazu, Chiba
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 TOIG of: ab037733 check: 4803 from: 1 to: 5139
 Locus AB037733 mRNA 5139 bp linear PRI 14-MAR-2000
 Definition Homo sapiens mRNA for KIAA1312 protein, partial cds.
 Accession AB037733 Version AB037733.1 GI:7242978
 Keywords SOURCE
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 clone_fh1767.
 Reference 1 (sites)
 Authors Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Title
 XVI. The complete sequences of 150 new cDNA clones from brain which
 code for large proteins in vitro
 Journal JOURNAL MEDLINE
 DNA Res. 7 (1), 65-73 (2000)
 MEDLINE
 20181126
 Reference 2 (bases 1 to 5139)
 Authors Ohara,O., Nagase,T. and Kikuno,R.
 Title Direct Submission
 Journal Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, China
 Laboratory of DNA Technology, 1512-3 Yana, Kasarazu, Chiba
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TOIG of: ab037733 check: 4803 from: 1 to: 5139

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VERSION AB037733.1
LOCUS AB037733
PRI 14-MAR-2000
DEFINITION Homo sapiens mRNA for KIAA1312 protein, partial cds.
VERSION AB037733.1
LOCUS AB037733
PRI 14-MAR-2000

Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
clone:fhl1767.

AUTHORS Nagase,T., Kikuno,R., Ishikawa,K.I., Hiroswa,M. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 150 new cDNA clones from brain which encode for known or predicted proteins.

JOURNAL
DNA Res., 7 (1), 65-73 (2000)
MEDLINE
20181126
REFERENCE
2 (bases 1 to 5139)
NUMBER
2

JOURNAL direct Submission
Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
laboratory of DNA Technology; 1535-3 Yana, Kisarazu, Chiba

URL: <http://www.kazusa.or.jp/huge/>, Tel: +81-438-52-3913,
Fax: +81-438-52-3914
Location/Qualifiers

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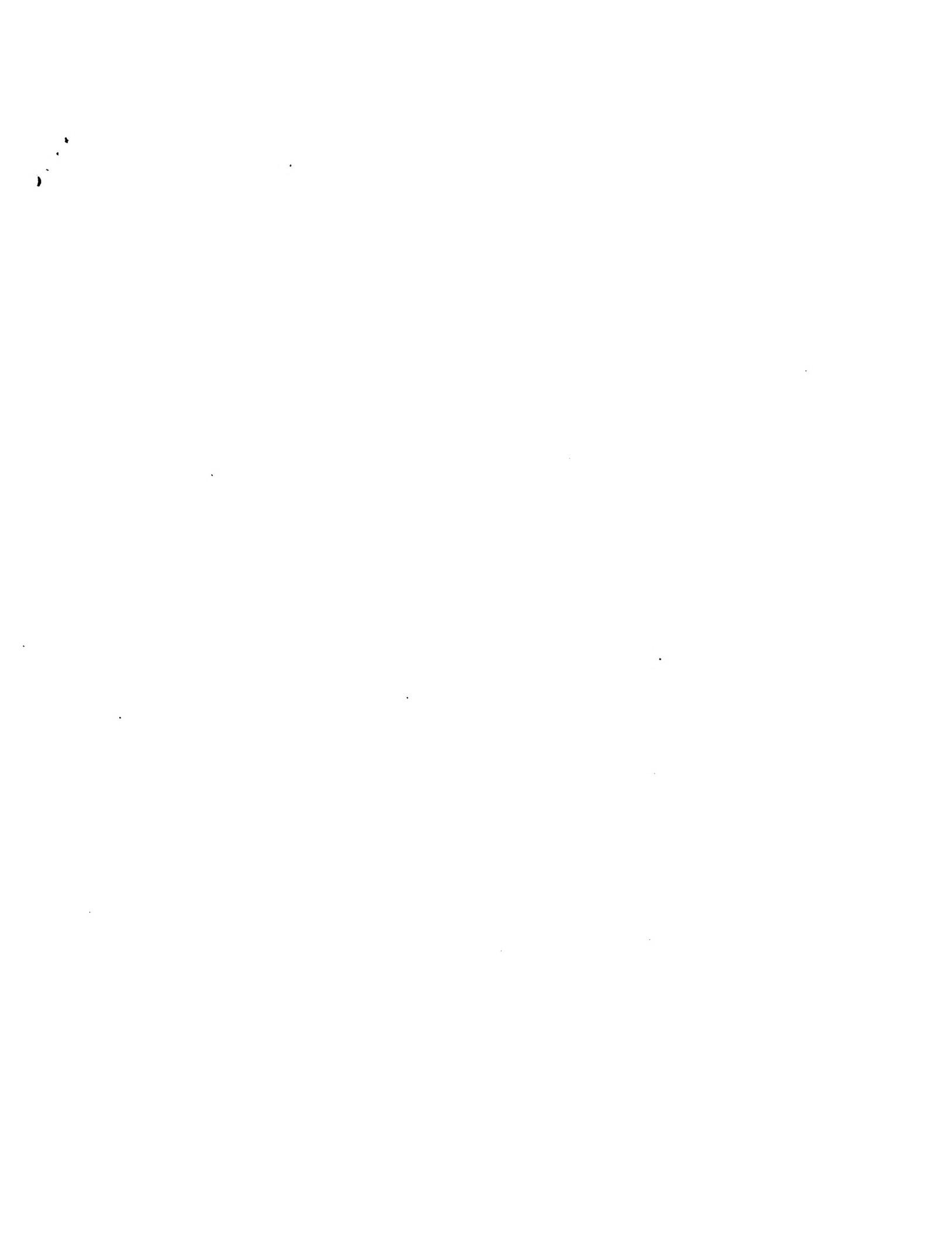
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1280	1290	1300	1310	1320	1330	1340
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1410	1420	1430	1440	1450	1460	1470
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5. US-09-972-467-2 (1-1629)
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 TOIG of: ab037733 check: 4803 from: 1 to: 5139

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Locus AB037733
 Definition Homo sapiens mRNA for KIA1312 protein, partial cds.
 Accession AB037733
 Version AB037733.1 GI:7242978

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ORGANISM	Homo sapiens	
REFERENCE	1 (sites)	
AUTHORS	Nagase,T., Kikuno,R., Ishikawa,K.I., Hirokawa,M. and Ohara,O.	
TITLE	Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro	
JOURNAL	DNA Res. 7 (1), 65-73 (2000)	
MEDLINE	20181126	
REFERENCE	2 (bases 1 to 5139)	
AUTHORS	Ohara,O., Nagase,T. and Kikuno,R.	
TITLE	Direct Submission	
JOURNAL	Submitted (1-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology, 1532-3 Yana, Kilarazu, Chiba 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp', URL: http://www.kazusa.or.jp/huge/, Tel.: +81-438-52-3913, Fax: +81-438-52-3914)	
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 TOIG of: ab037733 check: 4803 from: 1 to: 5139

Locus AB037733 5139 bp mRNA linear PRI 14-MAR-2000
 Definition Homo sapiens mRNA for KIAA1312 protein, partial cds.
 Accession AB037733
 Version AB037733.1 GI:74242978
 Keywords SOURCE
 Organism Homo sapiens brain cDNA to mRNA, clone_1.lib:pBluescriptII SK plus
 Clone:fhl1767.
 Mammal: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Authors Nagase,T., Kikuno,R., Ishikawa,K.I., Hirose,M. and Ohara,O.
 Title Prediction of the coding sequences of 150 new cDNA clones from brain which
 code for large proteins in Vitro
 Journal JOURNAL OF DNA TECHNOLOGY; 15(2-3) Yara, Kissarazu, Chiba
 MEDLINE 20181126
 Reference 1 (sites) 2000
 2 (bases 1 to 5139)
 Authors Ohara,O., Nagase,T. and Kikuno,R.
 Title Direct Submission
 Journal Submitted (31-JAN-2000) Ohara, Kazusa DNA Research Institute,
 laboratory of DNA Technology; 15(2-3) Yara, Kissarazu, Chiba
 URL: http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
 Fax:+81-438-52-3314
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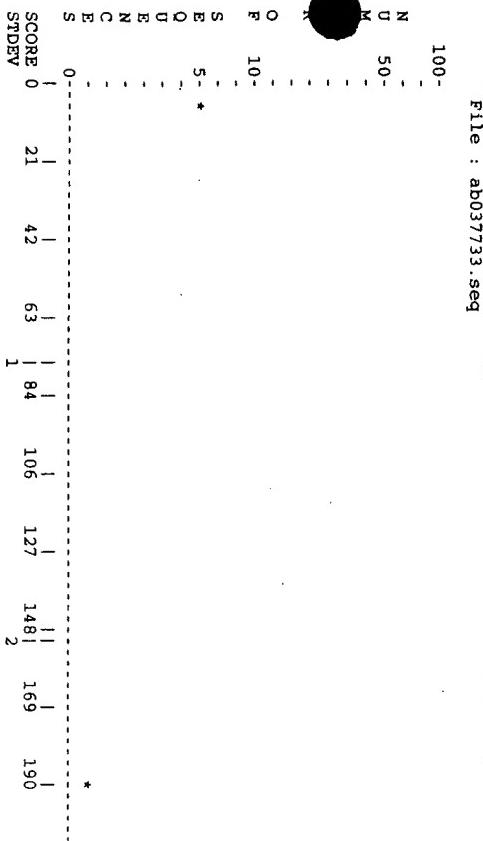
FastDB - Fast Pairwise Comparison of Sequences
 Release 5.4

Results file 09972467-2-289-478-ab037733.res made by jdelaval on Thu 20 Jun 102 6:16:17-

Query sequence being compared: US-09-972-467-2 (289-478)

Number of sequences searched: 6
 Number of scores above cutoff: 6

Results of the initial comparison of US-09-972-467-2 (289-478) with:
 File : ab037733.seq



Sequence Name	Description	Length	Score	Score	Sig.	Frame
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4. ab037733	TOIG of: ab037733	check: 480	1713	8	28	-0.39
5. ab037733	TOIG of: ab037733	check: 480	1711	7	37	-0.40
6. ab037733	TOIG of: ab037733	check: 480	1711	6	33	-0.42

The list of other best scores is:

Sequence Name	Description	Length	Init.	Opt.	Score	Sig.	Frame
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4. ab037733	TOIG of: ab037733	check: 480	1713	8	28	-0.39	1
5. ab037733	TOIG of: ab037733	check: 480	1711	7	37	-0.40	6
6. ab037733	TOIG of: ab037733	check: 480	1711	6	33	-0.42	5

TOIG of: ab037733 check: 4803 from: 1 to: 5139
 TOIG of: ab037733 check: 4803 from: 1 to: 5139

LOCUS AB037733 5139 bp mRNA linear PRI 14-MAR-2000
 DEFINITION Homo sapiens mRNA for KIAA1312 protein, partial cds.
 ACCESSION AB037733
 VERSION AB037733.1 GI:7242978

KEYWORDS Homo sapiens brain cDNA to mRNA, clone, lib:pBluescriptII SK plus
 SOURCE clone:fhl1767.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (sites)

REFERENCE Nagase,T., Kikuno,R., Ishikawa,K.I., Hiroswa,M. and Ohara,O.

AUTHORS Prediction of the coding sequences of unidentified human genes.

TITLE XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro

JOURNAL DNA Res. 7 (1), 65-73 (2000)

MEDLINE 2018126
 REFERENCE 2 (bases 1 to 5139)

AUTHORS Ohara,O., Nagase,T. and Kikuno,R.

TITLE Direct Submission

JOURNAL Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yara, Kisarazu, Chiba 292-0812, Japan (E-mail:cDNAinfo@kazusa.or.jp)
 URL: http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
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The scores below are sorted by initial score.
 Significance is calculated based on initial score.

A 100% similar sequence to the query sequence was found:

Init. Opt.



